



## SEQUENCE LISTING

<110> Himmler, Michele  
Schlokat, Uwe  
Baxter Aktiengesellschaft

<120> Factor X Analog With an Improved Ability to be  
Activated

<130> 20695C-005700US

<140> US 09/632.722

<141> 2000-08-04

<150> AT A1377/99

<151> 1999-08-10

<160> 18

<170> PatentIn Ver. 2.1

<210> 1

<211> 1467

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(1467)

<223> factor X

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Met Gly Arg Pro Leu His Leu Val Leu Leu Ser Ala Ser Leu Ala Gly  
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ctc ctg ctg ctc ggg gaa agt ctg ttc atc cgc agg gag cag gcc aac 96  
Leu Leu Leu Leu Gly Glu Ser Leu Phe Ile Arg Arg Glu Gln Ala Asn  
20 25 30

aac atc ctg gcg agg gtc acg agg gcc aat tcc ttt ctt gaa gag atg 144  
Asn Ile Leu Ala Arg Val Thr Arg Ala Asn Ser Phe Leu Glu Glu Met  
35 40 45

aag aaa gga cac ctc gaa aga gag tgc atg gaa gag acc tgc tca tac 192  
Lys Lys Gly His Leu Glu Arg Glu Cys Met Glu Glu Thr Cys Ser Tyr  
50 55 60

gaa gag gcc cgc gag gtc ttt gag gac agc gac aag acg aat gaa ttc 240  
Glu Glu Ala Arg Glu Val Phe Glu Asp Ser Asp Lys Thr Asn Glu Phe  
65 70 75 80

tgg aat aaa tac aaa gat ggc gac cag tgt gag acc agt cct tgc cag 288  
Trp Asn Lys Tyr Lys Asp Gly Asp Gln Cys Glu Thr Ser Pro Cys Gln  
85 90 95

aac cag ggc aaa tgt aaa gac ggc ctc ggg gaa tac acc tgc acc tgt 336  
Asn Gln Gly Lys Cys Lys Asp Gly Leu Gly Glu Tyr Thr Cys Thr Cys  
100 105 110

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TECH CENTER 1600/2900

tta gaa gga ttc gaa ggc aaa aac tgt gaa tta ttc aca cgg aag ctc	384
Leu Glu Gly Phe Glu Gly Lys Asn Cys Glu Leu Phe Thr Arg Lys Leu	
115 120 125	
tgc agc ctg gac aac ggg gac tgt gac cag ttc tgc cac gag gaa cag	432
Cys Ser Leu Asp Asn Gly Asp Cys Asp Gln Phe Cys His Glu Glu Gln	
130 135 140	
aac tct gtg gtg tgc tcc tgc gcc cgc ggg tac acc ctg gct gac aac	480
Asn Ser Val Val Cys Ser Cys Ala Arg Gly Tyr Thr Leu Ala Asp Asn	
145 150 155 160	
ggc aag gcc tgc att ccc aca ggg ccc tac ccc tgt ggg aaa cag acc	528
Gly Lys Ala Cys Ile Pro Thr Gly Pro Tyr Pro Cys Gly Lys Gln Thr	
165 170 175	
ctg gaa cgc agg aag agg tca gtg gcc cag gcc acc agc agc agc ggg	576
Leu Glu Arg Arg Lys Arg Ser Val Ala Gln Ala Thr Ser Ser Ser Gly	
180 185 190	
gag gcc cct gac agc atc aca tgg aag cca tat gat gca gcc gac ctg	624
Glu Ala Pro Asp Ser Ile Thr Trp Lys Pro Tyr Asp Ala Ala Asp Leu	
195 200 205	
gac ccc acc gag aac ccc ttc gac ctg ctt gac ttc aac cag acg cag	672
Asp Pro Thr Glu Asn Pro Phe Asp Leu Leu Asp Phe Asn Gln Thr Gln	
210 215 220	
cct gag agg ggc gac aac aac ctc acc agg atc gtg gga ggc cag gaa	720
Pro Glu Arg Gly Asp Asn Asn Leu Thr Arg Ile Val Gly Gly Gln Glu	
225 230 235 240	
tgc aag gac ggg gag tgt ccc tgg cag gcc ctg ctc atc aat gag gaa	768
Cys Lys Asp Gly Glu Cys Pro Trp Gln Ala Leu Leu Ile Asn Glu Glu	
245 250 255	
aac gag ggt ttc tgt ggt gga act att ctg agc gag ttc tac atc cta	816
Asn Glu Gly Phe Cys Gly Gly Thr Ile Leu Ser Glu Phe Tyr Ile Leu	
260 265 270	
acg gca gcc cac tgt ctc tac caa gcc aag aga ttc aag gtg agg gta	864
Thr Ala Ala His Cys Leu Tyr Gln Ala Lys Arg Phe Lys Val Arg Val	
275 280 285	
ggg gac cgg aac acg gag cag gag gag ggc ggt gag gcg gtg cac gag	912
Gly Asp Arg Asn Thr Glu Gln Glu Glu Gly Gly Glu Ala Val His Glu	
290 295 300	
gtg gag gtg gtc atc aag cac aac cgg ttc aca aag gag acc tat gac	960
Val Glu Val Val Ile Lys His Asn Arg Phe Thr Lys Glu Thr Tyr Asp	
305 310 315 320	
ttc gac atc gcc gtg ctc cgg ctc aag acc ccc atc acc ttc cgc atg	1008
Phe Asp Ile Ala Val Leu Arg Leu Lys Thr Pro Ile Thr Phe Arg Met	
325 330 335	
aac gtg gcg cct gcc tgc ctc ccc gag cgt gac tgg gcc gag tcc acg	1056
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[illegible]

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			20					25					30		
Asn	Ile	Leu	Ala	Arg	Val	Thr	Arg	Ala	Asn	Ser	Phe	Leu	Glu	Glu	Met
		35					40					45			
Lys	Lys	Gly	His	Leu	Glu	Arg	Glu	Cys	Met	Glu	Glu	Thr	Cys	Ser	Tyr
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Glu	Glu	Ala	Arg	Glu	Val	Phe	Glu	Asp	Ser	Asp	Lys	Thr	Asn	Glu	Phe
65					70					75					80
Trp	Asn	Lys	Tyr	Lys	Asp	Gly	Asp	Gln	Cys	Glu	Thr	Ser	Pro	Cys	Gln
				85					90					95	
Asn	Gln	Gly	Lys	Cys	Lys	Asp	Gly	Leu	Gly	Glu	Tyr	Thr	Cys	Thr	Cys
			100					105					110		

Leu Glu Gly Phe Glu Gly Lys Asn Cys Glu Leu Phe Thr Arg Lys Leu  
 115 120 125  
 Cys Ser Leu Asp Asn Gly Asp Cys Asp Gln Phe Cys His Glu Glu Gln  
 130 135 140  
 Asn Ser Val Val Cys Ser Cys Ala Arg Gly Tyr Thr Leu Ala Asp Asn  
 145 150 155 160  
 Gly Lys Ala Cys Ile Pro Thr Gly Pro Tyr Pro Cys Gly Lys Gln Thr  
 165 170 175  
 Leu Glu Arg Arg Lys Arg Ser Val Ala Gln Ala Thr Ser Ser Ser Gly  
 180 185 190  
 Glu Ala Pro Asp Ser Ile Thr Trp Lys Pro Tyr Asp Ala Ala Asp Leu  
 195 200 205  
 Asp Pro Thr Glu Asn Pro Phe Asp Leu Leu Asp Phe Asn Gln Thr Gln  
 210 215 220  
 Pro Glu Arg Gly Asp Asn Asn Leu Thr Arg Ile Val Gly Gly Gln Glu  
 225 230 235 240  
 Cys Lys Asp Gly Glu Cys Pro Trp Gln Ala Leu Leu Ile Asn Glu Glu  
 245 250 255  
 Asn Glu Gly Phe Cys Gly Gly Thr Ile Leu Ser Glu Phe Tyr Ile Leu  
 260 265 270  
 Thr Ala Ala His Cys Leu Tyr Gln Ala Lys Arg Phe Lys Val Arg Val  
 275 280 285  
 Gly Asp Arg Asn Thr Glu Gln Glu Glu Gly Gly Glu Ala Val His Glu  
 290 295 300  
 Val Glu Val Val Ile Lys His Asn Arg Phe Thr Lys Glu Thr Tyr Asp  
 305 310 315 320  
 Phe Asp Ile Ala Val Leu Arg Leu Lys Thr Pro Ile Thr Phe Arg Met  
 325 330 335  
 Asn Val Ala Pro Ala Cys Leu Pro Glu Arg Asp Trp Ala Glu Ser Thr  
 340 345 350  
 Leu Met Thr Gln Lys Thr Gly Ile Val Ser Gly Phe Gly Arg Thr His  
 355 360 365  
 Glu Lys Gly Arg Gln Ser Thr Arg Leu Lys Met Leu Glu Val Pro Tyr  
 370 375 380  
 Val Asp Arg Asn Ser Cys Lys Leu Ser Ser Ser Phe Ile Ile Thr Gln  
 385 390 395 400  
 Asn Met Phe Cys Ala Gly Tyr Asp Thr Lys Gln Glu Asp Ala Cys Gln  
 405 410 415  
 Gly Asp Ser Gly Gly Pro His Val Thr Arg Phe Lys Asp Thr Tyr Phe  
 420 425 430  
 Val Thr Gly Ile Val Ser Trp Gly Glu Ser Cys Ala Arg Lys Gly Lys  
 435 440 445  
 Tyr Gly Ile Tyr Thr Lys Val Thr Ala Phe Leu Lys Trp Ile Asp Arg  
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<210> 3

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<213> Artificial Sequence

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<223> Description of Artificial Sequence:PCR 5' primer  
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 protease cutting site in the region of the  
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<210> 8  
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<223> Description of Artificial Sequence:factor X  
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<211> 12

<212> PRT

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<223> Description of Artificial Sequence:factor X analog  
fX/fXIa(Q-R/I) protease cutting site in the region  
of the activation peptide

<400> 9

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<210> 10

<211> 10

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<223> Description of Artificial Sequence:factor X region  
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<210> 11

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modified in the activation peptide

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modified in the activation peptide

<400> 13

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<212> PRT

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<223> Description of Artificial Sequence:factor X analog  
modified in the activation peptide

<400> 14

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<211> 9

<212> PRT

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<223> Description of Artificial Sequence:factor X  
position 227-234

<400> 15

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<211> 9

<212> PRT

<213> Artificial Sequence

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modification in the region of amino acids 227-233

<400> 17  
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<210> 18  
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Ser Gln Thr Ser Lys Leu Thr  
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